Sequence Comparison A

SEQ ID NO: 1

```
RESULT   2
S30359
GTP-binding regulatory protein G alpha chain, phospholipase C-activating - turkey
N;Alternate names: phospholipase C-activating G protein
C;Species: Meleagris gallopavo (common turkey)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Feb-2001
C;Accession: S30359; S30360
R;Maurice, D.H.; Waldo, G.L.; Morris, A.J.; Nicholas, R.A.; Harden, T.K.
Biochem. J. 290, 765-770, 1993
A;Title: Identification of Galpha(11) as the phospholipase C-activating G-protein of
turkey erythrocytes.
A;Reference number: S30359; MUID:93207527
A;Accession: S30359
A;Molecule type: mRNA
A;Residues: 1-359 <MAU>
A;Cross-references: GB:X73072; NID:g312254; PIDN:CAA51530.1; PID:g312255
A;Experimental source: blood
A;Accession: S30360
A;Molecule type: protein
A;Residues: 78-92;121-132;158-180;253-256;307-312;339-345;355-359 <MAW>
A;Experimental source: erythrocytes
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;46-53/Region: nucleotide-binding motif A (P-loop)
F;156-158/Region: GTP-binding SAK/L motif
F;274-277/Region: GTP-binding NKXD motif
F;52/Binding site: GTP (Lys) #status predicted
F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted


  Query Match             82.0%;  Score 1507;  DB 2;  Length 359;
  Best Local Similarity   82.2%;  Pred. No. 4.6e-98;
  Matches  291;  Conservative   25;  Mismatches   36;  Indels    2;  Gaps    1;

Qy       1 MACCLSEEAREQKRINQEIEKQLQRDKRNARRELKLLLLGTGESGKSTFIKQMRIIHGQG 60
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Db       7 MACCLSDEVKESKRINAEIEKQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSG 66

Qy      61 YSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEELQEKAAVVREVDFESVTSF 120
           ||||||:   :|||||:| |:|||||||:|| | :  : |: :  | ::|||| | | :|
Db      67 YSEEDKKGFTKLVYQNIFTAMQSMIRAMETLKILY--KYEQNKANAVLIREVDVEKVMTF 124

Qy     121 EEPYVSYIKELWEDSGIQECYDRRREYQLTDSAKYYLSDLRRLAVPDYLPTEQDILRVRV 180
           |:|||| || || | |||||||||||||:|||||||||: |:| | ||||:||:|||||
Db     125 EQPYVSAIKTLWNDPGIQECYDRRREYQLSDSAKYYLSDVDRIATPGYLPTQQDVLRVRV 184

Qy     181 PTTGIIEYPFDLEQIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVECDN 240
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||| ||
Db     185 PTTGIIEYPFDLENIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDN 244

Qy     241 ENRMEESKALFRTIITYPWFTNSSVILFLNKKDLLEEKILYSHLADYFPEYDGPPRDPIA 300
           |||||||||||||||||||| ||||||||||||||:||||||| |||||:||| ||  |
Db     245 ENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEDKILYSHLVDYFPEFDGPQRDAQA 304

Qy     301 AREFILKMFVDLNPDADKIIYSHFTCATDTENIRFVFAAVKDTILQNNLKYIGL 354
           |||||||||||||:|||||||||||||||||||||||||||| |||   |
Db     305 AREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNL 358
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SEQ ID NO: 1

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RESULT   2
S30359
GTP-binding regulatory protein G alpha chain, phospholipase C-activating - turkey
N;Alternate names: phospholipase C-activating G protein
C;Species: Meleagris gallopavo (common turkey)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Feb-2001
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R;Maurice, D.H.; Waldo, G.L.; Morris, A.J.; Nicholas, R.A.; Harden, T.K.
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A;Title: Identification of Galpha(11) as the phospholipase C-activating G-protein of
turkey erythrocytes.
A;Reference number: S30359; MUID:93207527
A;Accession: S30359
A;Molecule type: mRNA
A;Residues: 1-359 <MAU>
A;Cross-references: GB:X73072; NID:g312254; PIDN:CAA51530.1; PID:g312255
A;Experimental source: blood
A;Accession: S30360
A;Molecule type: protein
A;Residues: 78-92;121-132;158-180;253-256;307-312;339-345;355-359 <MAW>
A;Experimental source: erythrocytes
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;46-53/Region: nucleotide-binding motif A (P-loop)
F;156-158/Region: GTP-binding SAK/L motif
F;274-277/Region: GTP-binding NKXD motif
F;52/Binding site: GTP (Lys) #status predicted
F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted


  Query Match             82.0%;  Score 1507;  DB 2;  Length 359;
  Best Local Similarity   82.2%;  Pred. No. 4.6e-98;
  Matches  291;  Conservative   25;  Mismatches   36;  Indels    2;  Gaps    1;

Qy       1 MACCLSEEAREQKRINQEIEKQLQRDKRNARRELKLLLLGTGESGKSTFIKQMRIIHGQG 60
           |||||:| :| |||| ||||||:||||:||||||||||||||||||||||||||||| |
Db       7 MACCLSDEVKESKRINAEIEKQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSG 66

Qy      61 YSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEELQEKAAVVREVDFESVTSF 120
           ||||||:   :|||||:| |:|||||||:|| | :  : |: :  | ::|||| | | :|
Db      67 YSEEDKKGFTKLVYQNIFTAMQSMIRAMETLKILY--KYEQNKANAVLIREVDVEKVMTF 124

Qy     121 EEPYVSYIKELWEDSGIQECYDRRREYQLTDSAKYYLSDLRRLAVPDYLPTEQDILRVRV 180
           |:|||| || || | |||||||||||||:|||||||||: |:| | ||||:||:|||||
Db     125 EQPYVSAIKTLWNDPGIQECYDRRREYQLSDSAKYYLSDVDRIATPGYLPTQQDVLRVRV 184

Qy     181 PTTGIIEYPFDLEQIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVECDN 240
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||
Db     185 PTTGIIEYPFDLENIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDN 244

Qy     241 ENRMEESKALFRTIITYPWFTNSSVILFLNKKDLLEEKILYSHLADYFPEYDGPPRDPIA 300
           |||||||||||||||||||| ||||||||||||||:||||||| |||||:||| ||  |
Db     245 ENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEDKILYSHLVDYFPEFDGPQRDAQA 304

Qy     301 AREFILKMFVDLNPDADKIIYSHFTCATDTENIRFVFAAVKDTILQNNLKYIGL 354
           |||||||||||||:|||||||||||||||||||||||||||| |||    |
Db     305 AREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNL 358


RESULT   1
Q17386
ID   Q17386      PRELIMINARY;      PRT;   355 AA.
AC   Q17386; O02546;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
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DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EGL-30 (HETEROTRIMERIC G PROTEIN ALPHA SUBUNIT).
GN   EGL-30 OR M01D7.7.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2;
RX   MEDLINE=96221161; PubMed=8630258;
RA   Brundage L., Avery L., Katz A., Kim U.J., Mendel J.E., Sternberg P.W.,
RA   Simon M.I.;
RT   "Mutations in a C. elegans Gqalpha gene disrupt movement, egg laying,
RT   and viability.";
RL   Neuron 16:999-1009(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA   Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Gattung S., Goela D., Wilson R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2;
RA   Cuppen E., Jansen G., Plasterk R.H.A.;
RT   "Interaction analysis of the complete G-alpha subfamily of
RT   heterotrimeric G proteins from Caenorhabditis elegans.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U56864; AAB04059.1; -.
DR   EMBL; AF003739; AAB58071.1; -.
DR   EMBL; AY008139; AAG32092.1; -.
DR   HSSP; P10824; 1BOF.
DR   InterPro; IPR001019; Gprotein_alpha.
DR   Pfam; PF00503; G-alpha; 1.
DR   PRINTS; PR00318; GPROTEINA.
DR   SMART; SM00275; G-alpha; 1.
SQ   SEQUENCE   355 AA;  41865 MW;  FEA38B01C2E1355C CRC64;


  Query Match             98.2%;  Score 1804;  DB 5;  Length 355;
  Best Local Similarity   98.9%;  Pred. No. 2.4e-116;
  Matches  350;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MACCLSEEAREQKRINQEIEKQLQRDKRNARRELKLLLLGTGESGKSTFIKQMRIIHGQG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MACCLSEEAREQKRINQEIEKQLQRDKRNARRELKLLLLGTGESGKSTFIKQMRIIHGQG 60

Qy      61 YSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEELQEKAAVVREVDFESVTSF 120
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Db      61 YSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEELQEKAAVVREVDFESVTSF 120

Qy     121 EEPYVSYIKELWEDSGIQECYDRRREYQLTDSAKYYLSDLRRLAVPDYLPTEQDILRVRV 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 EEPYVSYIKELWEDSGIQECYDRRREYQLTDSAKYYLSDLRRLAVPDYLPTEQDILRVRV 180

Qy     181 PTTGIIEYPFDLEQIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVECDN 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 PTTGIIEYPFDLEQIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVECDN 240

Qy     241 ENRMEESKALFRTIITYPWFTNSSVILFLNKKDLLEEKILYSHLADYFPEYDGPPRDPIA 300
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Db     241 ENRMEESKALFRTIITYPWFTNSSVILFLNKKDLLEEKILYSHLADYFPEYDGPPRDPIA 300

Qy     301 AREFILKMFVDLNPDADKIIYSHFTCATDTENIRFVFAAVKDTILQNNLKYIGL 354
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Db     301 AREFILKMFVDLNPDADKIIYSHFTCATDTENIRFVFAAVKDTILQHNLKEYNL 354
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1501	81.7	1276	20	AAY49127	phCaR/hmGluR2*Gqi5
2	1501	81.7	1323	20	AAY49133	GABA-BR1a*Gqo5 fus
3	1501	81.7	1394	20	AAY49129	pmGluR2/CaR*Galpha
4	1501	81.7	1397	20	AAY49134	pmGluR2/CaR*Galpha
5	1501	81.7	1418	20	AAY49131	mGluR8/CaR*Galphaq
6	1497	81.4	359	22	AAB99071	Human G-protein al
7	1497	81.4	359	22	AAB99073	Human G-protein al
8	1495	81.3	353	22	AAB99072	Human G-protein al
9	1494	81.3	1303	20	AAY49132	GABA-BR2*Gqo5 fusi
10	1493	81.2	359	20	AAY49125	Chimeric Gqi5 prot
11	1486	80.8	359	20	AAY52705	Human G-alpha-11 p
12	1486	80.8	359	20	AAY29789	Human G-alpha-11 p
13	1388	75.5	355	21	AAB15026	Mouse TC-Galpha14
14	1385	75.4	355	22	AAB99076	Human G-protein al
15	1029	56.0	374	22	AAB84005	Amino acid sequenc
16	1029	56.0	374	22	AAB84007	Amino acid sequenc
17	1028	55.9	374	22	AAB83997	Amino acid sequenc
18	1028	55.9	374	22	AAB83999	Amino acid sequenc
19	1028	55.9	374	22	AAB84001	Amino acid sequenc
20	1028	55.9	374	22	AAB84006	Amino acid sequenc
21	1028	55.9	374	22	AAB84008	Amino acid sequenc
22	1028	55.9	374	22	AAB84010	Amino acid sequenc
23	1027	55.9	374	22	AAB83978	Amino acid sequenc
24	1027	55.9	374	22	AAB83998	Amino acid sequenc
25	1027	55.9	374	22	AAB84000	Amino acid sequenc
26	1027	55.9	374	22	AAB84009	Amino acid sequenc
27	1024	55.7	374	22	AAB84002	Amino acid sequenc
28	1024	55.7	374	22	AAB84004	Amino acid sequenc
29	1023	55.7	374	22	AAB83996	Amino acid sequenc
30	1023	55.7	374	22	AAB84003	Amino acid sequenc
31	1020	55.5	374	22	AAB83990	Amino acid sequenc
32	1020	55.5	374	22	AAB83992	Amino acid sequenc
33	1019	55.4	374	22	AAB83982	Amino acid sequenc
34	1019	55.4	374	22	AAB83984	Amino acid sequenc
35	1019	55.4	374	22	AAB83986	Amino acid sequenc
36	1019	55.4	374	22	AAB83991	Amino acid sequenc
37	1019	55.4	374	22	AAB83993	Amino acid sequenc
38	1019	55.4	374	22	AAB83995	Amino acid sequenc
39	1018	55.4	374	22	AAB83977	Amino acid sequenc
40	1018	55.4	374	22	AAB83983	Amino acid sequenc
41	1018	55.4	374	22	AAB83985	Amino acid sequenc
42	1018	55.4	374	22	AAB83994	Amino acid sequenc
43	1015	55.2	374	22	AAB83987	Amino acid sequenc
44	1015	55.2	374	22	AAB83989	Amino acid sequenc
45	1014	55.2	374	22	AAB83981	Amino acid sequenc

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	98.2	355	2	T15288	hypothetical prote
2	1507	82.0	359	2	S30359	GTP-binding regula
3	1497	81.4	359	1	RGHUGY	GTP-binding regula
4	1495	81.3	359	2	S71963	GTP-binding protei
5	1490	81.1	359	1	RGMSQ	GTP-binding regula
6	1489	81.0	359	2	S45700	G-alpha-11 protein
7	1485	80.8	359	2	S45699	GTP-binding regula
8	1483	80.7	353	2	B40891	GTP-binding protei
9	1475	80.3	359	1	RGMS11	GTP-binding regula
10	1472	80.1	353	2	S34347	GTP-binding regula
11	1423.5	77.4	360	2	JN0115	GTP-binding regula
12	1388	75.5	355	2	A40891	GTP-binding protei
13	1388	75.5	355	2	A41534	GTP-binding protei
14	1370.5	74.6	354	2	S33309	GTP-binding regula
15	991	53.9	374	2	B41534	GTP-binding protei
16	965	52.5	374	2	A41096	GTP-binding regula
17	902	49.1	353	2	S71965	GTP-binding regula
18	901	49.0	355	2	I50238	Gi2 protein alpha-
19	896.5	48.8	354	2	S27014	GTP-binding regula
20	895	48.7	355	2	A61031	GTP-binding regula
21	894.5	48.7	354	1	RGHYO2	GTP-binding regula
22	894	48.6	355	1	RGHUI2	GTP-binding regula
23	893.5	48.6	354	1	RGHUO2	GTP-binding regula
24	892	48.5	355	2	S28158	GTP-binding regula
25	891.5	48.5	354	1	RGHUI1	GTP-binding regula
26	891.5	48.5	354	1	RGBOI1	GTP-binding regula
27	891.5	48.5	354	2	T19476	hypothetical prote
28	890.5	48.4	354	1	RGRTI1	GTP-binding regula
29	890	48.4	353	2	T50482	G protein alpha ch
30	887.5	48.3	354	1	RGMSO2	GTP-binding regula
31	887.5	48.3	354	2	A61035	GTP-binding regula
32	886	48.2	355	1	RGRTI2	GTP-binding regula
33	884.5	48.1	354	1	RGFFO2	GTP-binding regula
34	883.5	48.1	354	2	S40509	G-protein - chicke
35	882.5	48.0	354	1	RGRTO2	GTP-binding regula
36	881.5	48.0	354	2	I50237	GTP-binding regula
37	880.5	47.9	354	1	RGXLI1	GTP-binding regula
38	880	47.9	355	1	RGMSI2	GTP-binding regula
39	879.5	47.9	354	2	S28157	GTP-binding regula
40	877.5	47.7	354	2	S40508	GTP-binding regula
41	876.5	47.7	350	1	RGMST1	GTP-binding regula
42	875.5	47.6	354	2	S24362	GTP-binding regula
43	874.5	47.6	354	2	S27013	GTP-binding regula
44	872.5	47.5	354	1	RGFFO1	GTP-binding regula
45	871.5	47.4	350	1	RGBOT1	GTP-binding regula

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1522	82.8	353	1	GBQ3_DROME	P54400 drosophila
2	1507	82.0	359	1	GB11_MELGA	P45645 meleagris g
3	1497	81.4	353	1	GBQ_RAT	P82471 rattus norv
4	1496	81.4	353	1	GBQ_CANFA	Q28294 canis famil
5	1495	81.3	353	1	GBQ_HUMAN	P50148 homo sapien
6	1493	81.2	359	1	GB11_HUMAN	P29992 homo sapien
7	1490	81.1	353	1	GBQ_MOUSE	P21279 mus musculu
8	1489	81.0	359	1	GB11_XENLA	P43444 xenopus lae
9	1488	81.0	353	1	GBQ_HOMAM	P91950 homarus ame
10	1485	80.8	353	1	GBQ_XENLA	P38410 xenopus lae

11	1483	80.7	359	1	GB11_BOVIN	P38409	bos taurus
12	1475	80.3	359	1	GB11_MOUSE	P21278	mus musculu
13	1472	80.1	353	1	GBQ_LYMST	P38411	lymnaea sta
14	1470	80.0	359	1	GB11_RAT	Q9jid2	rattus norv
15	1452	79.0	353	1	GBQ_PATYE	O15975	patinopecte
16	1437	78.2	353	1	GBQ1_DROME	P23625	drosophila
17	1416	77.0	354	1	GB14_XENLA	O73819	xenopus lae
18	1388	75.5	355	1	GB14_BOVIN	P38408	bos taurus
19	1388	75.5	355	1	GB14_MOUSE	P30677	mus musculu
20	1385	75.4	355	1	GB14_HUMAN	O95837	homo sapien
21	1370.5	74.6	354	1	GBQ_LOLFO	P38412	loligo forb
22	991	53.9	374	1	GB15_MOUSE	P30678	mus musculu
23	990	53.9	374	1	GB15_RAT	O88302	rattus norv
24	965	52.5	374	1	GB15_HUMAN	P30679	homo sapien
25	901	49.0	352	1	GBA1_COCHE	O74227	cochliobolu
26	900	49.0	356	1	GB0_PATYE	O15976	patinopecte
27	897	48.8	352	1	GBA1_EMENI	Q00743	emericella
28	896	48.7	354	1	GBI2_CHICK	P50147	gallus gall
29	891.5	48.5	353	1	GB0_LYMST	P30683	lymnaea sta
30	890.5	48.4	353	1	GB0_HELTI	P51877	helisoma tr
31	890	48.4	352	1	GBA1_CRYPA	Q00580	cryphonectr
32	890	48.4	353	1	GBA1_NEUCR	Q05425	neurospora
33	890	48.4	354	1	GBI2_CANFA	P38400	canis famil
34	889.5	48.4	353	1	GB02_CRILO	P17806	cricetulus
35	889	48.4	354	1	GBI2_HUMAN	P04899	homo sapien
36	888.5	48.3	353	1	GB02_HUMAN	P29777	homo sapien
37	887.5	48.3	354	1	GB0_LOCMI	P38404	locusta mig
38	886.5	48.2	353	1	GBI1_HUMAN	P04898	homo sapien
39	885.5	48.2	353	1	GBI1_RAT	P10824	rattus norv
40	884	48.1	352	1	GBA1_COLTR	O42784	colletotric
41	884	48.1	352	1	GBA1_SPOSC	O74259	sporothrix
42	883	48.0	354	1	GBI2_CAVPO	P38402	cavia porce
43	882.5	48.0	353	1	GB02_MOUSE	P18873	mus musculu
44	881	47.9	352	1	GBA1_MAGGR	O13315	magnaporthe
45	881	47.9	354	1	GBI2_RAT	P04897	rattus norv